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Tina Dasco
(Print Name)

Date: 1-7-00

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(Signature)

PATENT APPLICATION

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application

Batch No. 435-188.000
Notice of Allowance Date: 10/6/99

Inventor's Name(s): Gelfand et al.

Art Unit: 1651

Serial No. 07/873,897, filed April 24, 1992

Examiner: D. Naff

For: **PURIFIED THERMOSTABLE ENZYME**

TRANSMITTAL OF FORMAL DRAWINGS

Assistant Commissioner for Patents
Washington, D.C. 20231

Alameda, CA
January 6, 2000

Sir:

Enclosed are the formal drawings (eight sheets) for filing in the above-identified U.S. Patent Application.

Respectfully submitted,

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Enclosures (Figs. 1-8)

6127155

TAQ DNA POLYMERASE SEQUENCE FIG.1-1

```
-120                -100                -80
      BglII                          PvuII
AAGCTCAGATCTACCTGCCTGAGGGCGTCCGGTTCCAGCTGGCCCTTCCCGAGGGGGAGA

-60                 -40                 -20
GGGAGGCGTTTCTAAAAGCCCTTCAGGACGCTACCCGGGGGCGGGTGGTGGAAGGGTAAC

1                   20                  40                  60
ATGAGGGGGATGCTGCCCCTCTTTGAGCCCAAGGGCCGGGTCCTCCTGGTGGACGGCCAC
MetArgGlyMetLeuProLeuPheGluProLysGlyArgValLeuLeuValAspGlyHis
  1

                    80                  100                 120
CACCTGGCCTACCGCACCTTCCACGCCCTGAAGGGCCTCACCACCAGCCGGGGGGAGCCG
HisLeuAlaTyrArgThrPheHisAlaLeuLysGlyLeuThrThrSerArgGlyGluPro

                   140                 160                 180
GTGCAGGCGGTCTACGGCTTCGCCAAGAGCCTCCTCAAGGCCCTCAAGGAGGACGGGGAC
ValGlnAlaValTyrGlyPheAlaLysSerLeuLeuLysAlaLeuLysGluAspGlyAsp
 41

                   200                 220                 240
GCGGTGATCGTGGTCTTTGACGCCAAGGCCCCCTCCTTCCGCCACGAGGCCTACGGGGGG
AlaValIleValValPheAspAlaLysAlaProSerPheArgHisGluAlaTyrGlyGly

                   260                 280                 300
TACAAGGCGGGCCGGGCCCCCACGCCGGAGGACTTTCCCCGGCAACTCGCCCTCATCAAG
TyrLysAlaGlyArgAlaProThrProGluAspPheProArgGlnLeuAlaLeuIleLys
 81

                   320                 340                 360
                                  XhoI
GAGCTGGTGGACCTCCTGGGGCTGGCGCGCCTCGAGGTCCCGGGCTACGAGGCGGACGAC
GluLeuValAspLeuLeuGlyLeuAlaArgLeuGluValProGlyTyrGluAlaAspAsp
```

TAQ DNA POLYMERASE SEQUENCE

FIG.1-2

```
                    380                 400                 420
GTCCTGGCCAGCCTGGCCAAGAAGGCGGAAAAGGAGGGCTACGAGGTCCGCATCCTCACC
ValLeuAlaSerLeuAlaLysLysAlaGluLysGluGlyTyrGluValArgIleLeuThr
121

                    440                 460                 480
GCCGACAAAGACCTTTACCAGCTCCTTTCCGACCGCATCCACGTCCTCCACCCCGAGGGG
AlaAspLysAspLeuTyrGlnLeuLeuSerAspArgIleHisValLeuHisProGluGly

                    500                 520                 540
Asp718
TACCTCATCACCCCGGCCTGGCTTTGGGAAAAGTACGGCCTGAGGCCCGACCAGTGGGCC
TyrLeuIleThrProAlaTrpLeuTrpGluLysTyrGlyLeuArgProAspGlnTrpAla
161

                    560                 580                 600
GACTACCGGGCCCTGACCGGGGACGAGTCCGACAACCTTCCCGGGGTCAAGGGCATCGGG
AspTyrArgAlaLeuThrGlyAspGluSerAspAsnLeuProGlyValLysGlyIleGly

                    620                 640                 660
                HindIII
GAGAAGACGGCGAGGAAGCTTCTGGAGGAGTGGGGGAGCCTGGAAGCCCTCCTCAAGAAC
GluLysThrAlaArgLysLeuLeuGluGluTrpGlySerLeuGluAlaLeuLeuLysAsn
201

                    680                 700                 720
CTGGACCGGCTGAAGCCCGCCATCCGGGAGAAGATCCTGGCCCACATGGACGATCTGAAG
LeuAspArgLeuLysProAlaIleArgGluLysIleLeuAlaHisMetAspAspLeuLys

                    740                 760                 780
CTCTCCTGGGACCTGGCCAAGGTGCGCACCGACCTGCCCCTGGAGGTGGACTTCGCCAAA
LeuSerTrpAspLeuAlaLysValArgThrAspLeuProLeuGluValAspPheAlaLys
241

                    800                 820                 840
AGGCGGGAGCCCGACCGGGAGAGGCTTAGGGCCTTTCTGGAGAGGCTTGAGTTTGGCAGC
ArgArgGluProAspArgGluArgLeuArgAlaPheLeuGluArgLeuGluPheGlySer
```

TAQ DNA POLYMERASE SEQUENCE

FIG.1-3

```
                    860                 880                 900
                                      BstXI
CTCCTCCACGAGTTCGGCCTTCTGGAAAGCCCCAAGGCCCTGGAGGAGGCCCCCTGGCCC
LeuLeuHisGluPheGlyLeuLeuGluSerProLysAlaLeuGluGluAlaProTrpPro
281                             290

                    920                 940                 960
CCGCCGGAAGGGGCCTTCGTGGGCTTTGTGCTTTCCCGCAAGGAGCCCATGTGGGCCGAT
ProProGluGlyAlaPheValGlyPheValLeuSerArgLysGluProMetTrpAlaAsp

                    980                1000                1020
CTTCTGGCCCTGGCCGCCGCCAGGGGGGGCCGGGTCCACCGGGCCCCCGAGCCTTATAAA
LeuLeuAlaLeuAlaAlaAlaArgGlyGlyArgValHisArgAlaProGluProTyrLys
321

                   1040                1060                1080
GCCCTCAGGGACCTGAAGGAGGCGCGGGGGCTTCTCGCCAAAGACCTGAGCGTTCTGGCC
AlaLeuArgAspLeuLysGluAlaArgGlyLeuLeuAlaLysAspLeuSerValLeuAla

                   1100                1120                1140
CTGAGGGAAGGCCTTGGCCTCCCGCCCGGCGACGACCCCATGCTCCTCGCCTACCTCCTG
LeuArgGluGlyLeuGlyLeuProProGlyAspAspProMetLeuLeuAlaTyrLeuLeu
361

                   1160                1180                1200
GACCCTTCCAACACCACCCCCGAGGGGGTGGCCCGGCGCTACGGCGGGGAGTGGACGGAG
AspProSerAsnThrThrProGluGlyValAlaArgArgTyrGlyGlyGluTrpThrGlu

                   1220                1240                1260
GAGGCGGGGGAGCGGGCCGCCCTTTCCGAGAGGCTCTTCGCCAACCTGTGGGGGAGGCTT
GluAlaGlyGluArgAlaAlaLeuSerGluArgLeuPheAlaAsnLeuTrpGlyArgLeu
401

                   1280                1300                1320
GAGGGGGAGGAGAGGCTCCTTTGGCTTTACCGGGAGGTGGAGAGGCCCCTTTCCGCTGTC
GluGlyGluGluArgLeuLeuTrpLeuTyrArgGluValGluArgProLeuSerAlaVal
```

TAQ DNA POLYMERASE SEQUENCE

FIG.1-4

1340 1360 1380

CTGGCCCACATGGAGGCCACGGGGGTGCGCCTGGACGTGGCCTATCTCAGGGCCTTGTCC
LeuAlaHisMetGluAlaThrGlyValArgLeuAspValAlaTyrLeuArgAlaLeuSer
441

1400 1420 1440

XhoI

CTGGAGGTGGCCGAGGAGATCGCCCGC*CTCGAG*GCCGAGGTCTTCCGCCTGGCCGGCCAC
LeuGluValAlaGluGluIleAlaArgLeuGluAlaGluValPheArgLeuAlaGlyHis

1460 1480 1500

PvuII

CCCTTCAACCTCAACTCCCGGGAC*CAGCTG*GAAAGGGTCCTCTTTGACGAGCTAGGGCTT
ProPheAsnLeuAsnSerArgAspGlnLeuGluArgValLeuPheAspGluLeuGlyLeu
481

1520 1540 1560

CCCGCCATCGGCAAGACGGAGAAGACCGGCAAGCGCTCCACCAGCGCCGCCGTCCTGGAG
ProAlaIleGlyLysThrGluLysThrGlyLysArgSerThrSerAlaAlaValLeuGlu

1580 1600 1620

PstI *SacI*

GCCCTCCGCGAGGCCCACCCCATCGTGGAGAAGATC*CTGCAG*TACCGG*GAGCTC*ACCAAG
AlaLeuArgGluAlaHisProIleValGluLysIleLeuGlnTyrArgGluLeuThrLys
521

1640 1660 1680

CTGAAGAGCACCTACATTGACCCCTTGCCGGACCTCATCCACCCCAGGACGGGCCGCCTC
LeuLysSerThrTyrIleAspProLeuProAspLeuIleHisProArgThrGlyArgLeu

1700 1720 1740

CACACCCGCTTCAACCAGACGGCCACGGCCACGGGCAGGCTAAGTAGCTCCGATCCCAAC
HisThrArgPheAsnGlnThrAlaThrAlaThrGlyArgLeuSerSerSerAspProAsn
561

1760 1780 1800

BamHI

CTCCAGAACATCCCCGTCCGCACCCCGCTTGGGCAGA*GGATCC*GCCGGGCCTTCATCGCC
LeuGlnAsnIleProValArgThrProLeuGlyGlnArgIleArgArgAlaPheIleAla

TAQ DNA POLYMERASE SEQUENCE

FIG.1-5

1820 1840 1860

SacI

GAGGAGGGGTGGCTATTGGTGGCCCTGGACTATAGCCAGATA*GAGCTC*AGGGTGCTGGCC
GluGluGlyTrpLeuLeuValAlaLeuAspTyrSerGlnIleGluLeuArgValLeuAla
601

1880 1900 1920

CACCTCTCCGGCGACGAGAACCTGATCCGGGTCTTCCAGGAGGGGCGGGACATCCACACG
HisLeuSerGlyAspGluAsnLeuIleArgValPheGlnGluGlyArgAspIleHisThr

1940 1960 1980

PvuII

GAGACCGC*CAGCTG*GATGTTCGGCGTCCCCCGGGAGGCCGTGGACCCCCTGATGCGCCGG
GluThrAlaSerTrpMetPheGlyValProArgGluAlaValAspProLeuMetArgArg
641

2000 2020 2040

GCGGCCAAGACCATCAACTTCGGGGTCCTCTACGGCATGTCGGCCCACCGCCTCTCCCAG
AlaAlaLysThrIleAsnPheGlyValLeuTyrGlyMetSerAlaHisArgLeuSerGln

2060 2080 2100

NheI

GA*GCTAGC*CATCCCTTACGAGGAGGCCCAGGCCTTCATTGAGCGCTACTTTCAGAGCTTC
GluLeuAlaIleProTyrGluGluAlaGlnAlaPheIleGluArgTyrPheGlnSerPhe
681

2120 2140 2160

CCCAAGGTGCGGGCCTGGATTGAGAAGACCCTGGAGGAGGGCAGGAGGCGGGGGTACGTG
ProLysValArgAlaTrpIleGluLysThrLeuGluGluGlyArgArgArgGlyTyrVal

2180 2200 2220

GAGACCCTCTTCGGCCGCCGCCGCTACGTGCCAGACCTAGAGGCCCGGGTGAAGAGCGTG
GluThrLeuPheGlyArgArgArgTyrValProAspLeuGluAlaArgValLysSerVal
721

TAQ DNA POLYMERASE SEQUENCE

2240 2260 2280

CGGGAGGCGGCCGAGCGCATGGCCTTCAACATGCCCGTCCAGGGCACCGCCGCCGACCTC
ArgGluAlaAlaGluArgMetAlaPheAsnMetProValGlnGlyThrAlaAlaAspLeu
741

2300 2320 2340

ATGAAGCTGGCTATGGTGAAGCTCTTCCCCAGGCTGGAGGAAATGGGGGCCAGGATGCTC
MetLysLeuAlaMetValLysLeuPheProArgLeuGluGluMetGlyAlaArgMetLeu

2360 2380 2400

XhoI

CTTCAGGTCCACGACGAGCTGGTC*CTCGAG*GCCCCAAAAGAGAGGGCGGAGGCCGTGGCC
LeuGlnValHisAspGluLeuValLeuGluAlaProLysGluArgAlaGluAlaValAla
781

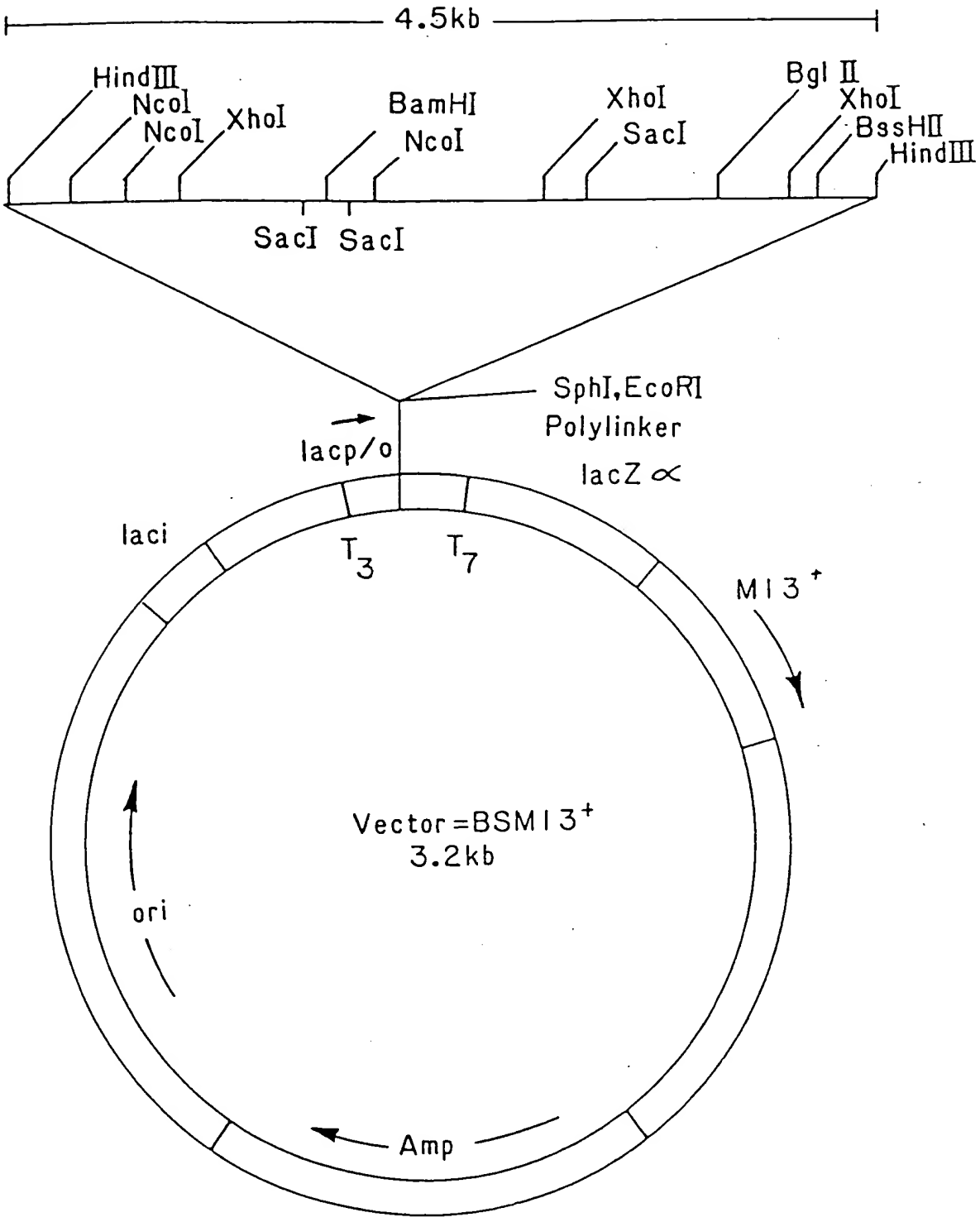
2420 2440 2460

CGGCTGGCCAAGGAGGTCATGGAGGGGGTGTATCCCCTGGCCGTGCCCCTGGAGGTGGAG
ArgLeuAlaLysGluValMetGluGlyValTyrProLeuAlaValProLeuGluValGlu

2480 2500

GTGGGGATAGGGGAGGACTGGCTCTCCGCCAAGGAGTGATACCACC
ValGlyIleGlyGluAspTrpLeuSerAlaLysGluEnd
821 832

FIG.1-6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SacI
SacI
SphI, EcoRI
Polylinker
lacp/o
lacZ ∝
laci
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T7
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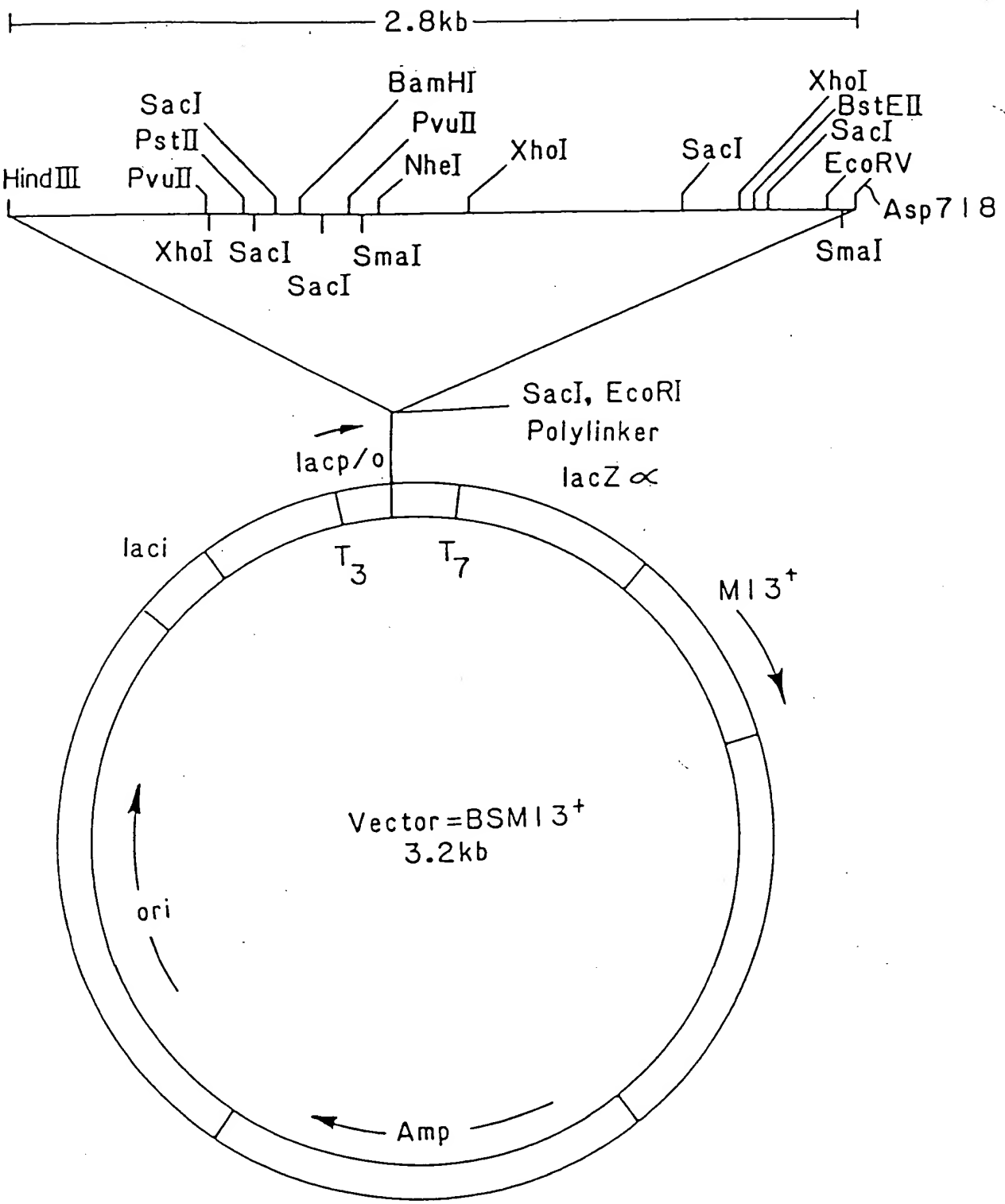
ori
Amp

FIG.2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HindIII
PvuII
BamHI
PvuII
NheI
XhoI
SacI
XhoI
BstEII
SacI
EcoRV
Asp718
XhoI
SacI
SacI
SmaI
SmaI
SacI, EcoRI
Polylinker
lacp/o
lacZ∝
laci
T3
T7
M13+
Vector=BSM13+
3.2kb
ori
Amp

FIG.3